This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)     General Information:                    ENTERED
 4
 5      (i) APPLICANT: Caras, Ingrid W
 6
 7     (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor
 8
 9    (iii) NUMBER OF SEQUENCES: 8
10
11     (iv) CORRESPONDENCE ADDRESS:
12          (A) ADDRESSEE: Genentech, Inc.
13          (B) STREET: 460 Point San Bruno Blvd
14          (C) CITY: South San Francisco
15          (D) STATE: California
16          (E) COUNTRY: USA
17          (F) ZIP: 94080
18
19      (v) COMPUTER READABLE FORM:
20          (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21          (B) COMPUTER: IBM PC compatible
22          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23          (D) SOFTWARE: WinPatin (Genentech)
24
25     (vi) CURRENT APPLICATION DATA:
26          (A) APPLICATION NUMBER: 08/635130
27          (B) FILING DATE: 19-Mar-1996
28          (C) CLASSIFICATION:
29
30   (viii) ATTORNEY/AGENT INFORMATION:
31          (A) NAME: Torchia, PhD., Timothy E.
32          (B) REGISTRATION NUMBER: 36,700
33          (C) REFERENCE/DOCKET NUMBER: P1001
34
35     (ix) TELECOMMUNICATION INFORMATION:
36          (A) TELEPHONE: 415/225-8674
37          (B) TELEFAX: 415/952-9881
38          (C) TELEX: 910/371-7168
39
40   (2) INFORMATION FOR SEQ ID NO:1:
41
42     (i) SEQUENCE CHARACTERISTICS:
43          (A) LENGTH: 1877 base pairs
44          (B) TYPE: Nucleic Acid
45          (C) STRANDEDNESS: Double
46          (D) TOPOLOGY: Linear
```

INPUT SET: S11899.raw

```
47
48    (ix) FEATURE:
49          (A) NAME/KEY: Extra Cellular Domain
50          (B) LOCATION: 244-899
51          (C) IDENTIFICATION METHOD:
52          (D) OTHER INFORMATION:
53
54    (ix) FEATURE:
55          (A) NAME/KEY: Transmembrane Domain
56          (B) LOCATION: 901-978
57          (C) IDENTIFICATION METHOD:
58          (D) OTHER INFORMATION:
59
60    (ix) FEATURE:
61          (A) NAME/KEY: signal peptide
62          (B) LOCATION: 244-321
63          (C) IDENTIFICATION METHOD:
64          (D) OTHER INFORMATION:
65
66     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68
69    GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCT 50
70
71    GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
72.
73    CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
74
75    CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
76
77    TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGGCGGG GTC ATG 246
78                                                    Met
79                                                     1
80
81    GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
82    Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
83                 5                   10
84
85    GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
86    Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
87     15              20                  25
88
89    CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
90    Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
91              30                  35                  40
92
93    AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
94    Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
95                     45                  50
96
97    ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
98    Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
99         55                  60                  65
```

```
100
101   CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
102   Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
103               70                  75
104
105   AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
106   Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
107    80                  85                  90
108
109   GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
110   Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
111            95                  100                 105
112
113   CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
114   Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
115                 110                 115
116
117   GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
118   Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
119         120                 125                 130
120
121   CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
122   His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr
123                 135                 140
124
125   CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
126   Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
127   145                 150                 155
128
129   ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
130   Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
131            160                 165                 170
132
133   CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
134   Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
135                 175                 180
136
137   ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
138   Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
139         185                 190                 195
140
141   GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
142   Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
143            200                 205
144
145   AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
146   Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
147   210                 215                 220
148
149   CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
150   Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
151         225                 230                 235
152
```

INPUT SET: S11899.raw

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153   GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
154   Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala
155                   240                 245
156
157   ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026
158   Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser
159       250                 255                 260
160
161   CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065
162   Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser
163                   265                 270
164
165   CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG 1104
166   Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu
167   275                 280                 285
168
169   GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143
170   Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
171                   290                 295                 300
172
173   GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182
174   Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys
175                   305                 310
176
177   GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221
178   Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
179       315                 320                 325
180
181   GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260
182   Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr
183                   330                 335
184
185   TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299
186   Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile
187   340                 345                 350
188
189   CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
190   Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
191       355                 360                 365
192
193   ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
194   Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
195                   370                 375
196
197   TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
198   Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
199       380                 385                 390
200
201   TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
202   Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
203                   395                 400
204
205   ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494
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PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/635,130*

DATE: 08/01/96
TIME: 14:41:18

INPUT SET: S11899.raw

```
206  Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr
207  405             410             415

208

209  GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT CTT GGG AGG 1533
210  Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
211      420             425               430

212

213  CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
214  Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
215              435             440

216

217  AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
218  Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
219      445             450             455

220

221  ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660

222

223  GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710

224

225  CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760

226

227  TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810

228

229  CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTCGA TATCAAGCTT 1860

230

231  ATCGATACCG TCGACCT 1877

232

233  (2) INFORMATION FOR SEQ ID NO:2:

234

235      (i) SEQUENCE CHARACTERISTICS:
236          (A) LENGTH: 455 amino acids
237          (B) TYPE: Amino Acid
238          (D) TOPOLOGY: Linear

239

240      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

241

242  Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
243   1             5               10                  15

244

245  Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
246              20              25              30

247

248  Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
249              35              40              45

250

251  Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
252              50              55              60

253

254  Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
255              65              70              75

256

257  Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
258              80              85              90
```

INPUT SET: S11899.raw

Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/635130